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135

140

19/75

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	576 Gly	Val	Glu	Val	Arg	Val	Trp	Asp		Thr	Ala	Glu	Leu	_	Tyr	Leu
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Glu Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Arg Ile Val Glu Ala 35 40 45

30

50

Phe Glu Thr Arg Ile Gly Pro His Ile Gly Ala Arg Ile Val Ala Arg 50 55 60

35
Ala Trp Ala Asp Ala Glu Phe Lys Arg Arg Leu Leu Ala Asp Ala Thr
65
70
75
80

40 Glu Ala Ala Asn Ser Leu Gly His Ala Ser Pro Val Gly Ser His Leu 85 90 95

Ile Ala Val Glu Asn Thr Pro Gln Thr His Asn Leu Val Val Cys Thr 100 105 110

Leu Cys Ser Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp 115 120 125

Tyr Lys Ser Ala Ala Tyr Arg Ser Arg Val Val Ile Asp Pro Lys Gly 130 135 140 .

Val Leu Ala Glu Phe Gly Leu Thr Leu Pro Pro Glu Thr Gly Ile Arg 145 150 155 160 23/75

Ile Trp Asp Ser Thr Ala Glu Thr Arg Phe Leu Val Val Pro Met Arg 165 170 175 5 Pro Pro Gly Thr Ala Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Val 180 185 190 Thr Arg Asp Ser Met Ile Gly Thr Gly Leu Ala Gly Ala Pro Gln Glu 10 195 200 205 Met Ala Ser Ala 210 15 <210> 45 <211> 696 <212> DNA 20 <213> Unknown <220> <223> Metagenome - alpha unit nitrile hydratase - M15aA6 25 <220> <221> CDS (1)..(696)<222> <223> 30 <400> 45 atg cgt tcg ccc ggt gag gcc tca gca acg caa cca gcg ctc att cgg 48 Met Arg Ser Pro Gly Glu Ala Ser Ala Thr Gln Pro Ala Leu Ile Arg 10 1 15 35 ctg cat gat cga gct ggc gtt cga tca ttg cgc ggc aaa agg tct 96 Leu His Asp Arg Ala Gly Gly Val Arg Ser Leu Arg Gly Lys Arg Ser 20 25 30 40 cat cgc gcc gga tcg cat cct cgg ggc gct cgc gca tcc gtc gcc aca 144 His Arg Ala Gly Ser His Pro Arg Gly Ala Arg Ala Ser Val Ala Thr 35 40 45 ggg tgg ttc gtt ccg ttc tcg gcc agg ctc gcc cgg aaa ggc atc gct 192 Gly Trp Phe Val Pro Phe Ser Ala Arg Leu Ala Arg Lys Gly Ile Ala 55 50 60 50 cct ccg gcc gag atc gcc gag cgg atc gcc gtc acc gat cgc gca tca 240 Pro Pro Ala Glu Ile Ala Glu Arg Ile Ala Val Thr Asp Arg Ala Ser 65 70 75 80 55 ccg gca atg ggc gct cgc atg gtc gcc aag gcc tgg acc gat ccc gcc 288 Pro Ala Met Gly Ala Arg Met Val Ala Lys Ala Trp Thr Asp Pro Ala 85 90 95

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	His	Arg	Ala 35	Gly	Ser	His	Pro	Arg 40	Gly	Ala	Arg	Ala	Ser 45	Val	Ala	Thr
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F 0	Asp	Tyr	Arg 195	Trp	Met	Val	Leu	Pro 200	Val	Arg	Pro	Ala	Gly 205	Thr	Ala	Gly
50	Trp	Asp 210	Glu	Glu	Arg	Leu	Ala 215	Ala	Ile	Val	Arg	Glu 220	Gly	Asp	Met	Ile
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135

130

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Asp Phe Gly Leu Lys Leu Ala Pro Asp Met Gln Ile Arg Val Trp Asp

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55	Lys	Gly	Leu 35	Ile	Ala	Thr	Asp	Val 40	Ile	Asp	Arg	Val	Val 45	Ala	Thr	Tyr
	.a. 7	_	en 7	4	~- T	_	•••	-	~3	- 4	_	~~ 7	~ ~ ~ ~	T	70	~ 4

Glu Lys Glu Val Gly Pro Leu Asn Gly Ala Lys Val Val Ala Arg Ala

30/75

Trp Thr Asp Pro Glu Tyr Arg Arg Leu Leu Lys Asn Gly Thr Ala Ala Ile Ala Glu Leu Gly Phe Gly Gly Leu Gln Gly Glu His Met Met Val Val Glu Asn Thr Pro Ser Val His Asn Val Ile Cys Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ser Trp Tyr Lys Ser Leu Ala Tyr Arg Ser Arg Ile Val Arg Glu Pro Arg Ala Val Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu Thr Val Glu Val Arg Val Trp Asp Ser Ser Ala Glu Met Arg Tyr Leu Val Leu Pro Glu Arg Pro Ala Gly Thr Thr Glu Leu Ser Glu Ala Glu Leu Ala Ser Leu Ile Thr Arg Asp Ala Leu Ile Gly Val Ala Lys Val Ala Ala Pro Ser Arg <210> <211> <212> DNA <213> Unknown <220> Metagenome - alpha unit nitrile hydratase - M6dE2 <223> <220> <221> CDS <222> (1)..(600)<223> <400> atg agc aac cca cgc cgt cga gaa cgg tcg gcc cca ccg gat gcg cga Met Ser Asn Pro Arg Arg Glu Arg Ser Ala Pro Pro Asp Ala Arg

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	240 Arg	_	_											Ala		
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	288						gag							gac		ctg
25	т <i></i> Ут	ALA	Gry	110	85	CTJ	OLU	* <u>*</u> *	110	90	vai	110a	OIA	riop	95	БСС
	336													act		
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10	Arg	Val	Val	Ala	Arg 85	Ala	Trp	Val	Asp	Pro 90	Asp	Tyr	Lys	Gln	Arg 95	Leu
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20	Gln	Gly	Ala 115	Asp	Ile	Arg	Val	Val 120	Glu	Asn	Thr	Ala	Thr 125	Val	His	Asn
0.5	Leu	Val 130	Val	Cys	Thr	Leu	Cys 135	Ser	Cys	Tyr	Pro	Trp 140	Pro	Val	Leu	Gly
25	Leu 145	Pro	Pro	Val	Trp	Tyr 150	Lys	Ser	Ala	Pro	Tyr 155	Arg	Ser	Arg	Val	Val 160
30	Ile	Asp	Pro	Arg	Gly 165	Val	Leu	Arg	Glu	Phe 170	Gly	Val	Val	Leu	Pro 175	Asp
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 Tyr Tyr Gln Met Met Glu Val Ser Leu Arg Glu Leu Leu Val Glu Lys 20
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 Gly Val Ile Thr Glu Ala Glu Val Ala Arg Ala Met Gly Glu Ile Gly 35
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 45
- 20 gcg aga agc ccg gag cgc gcg aag atg gtc gcg cgc gcg tgg gtg 192 Ala Arg Ser Pro Glu Arg Gly Ala Lys Met Val Ala Arg Ala Trp Val 50
- gac ccg gcg tac aag gcg cgc atg ctt gcc gac ggc agc aag gcc gcc 240
 Asp Pro Ala Tyr Lys Ala Arg Met Leu Ala Asp Gly Ser Lys Ala Ala 65
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 80
- 30 gag gag ctc ggg ttc gag gtg ccg ggc ctc aag ctg atc gtg gtc gag 288
 Glu Glu Leu Gly Phe Glu Val Pro Gly Leu Lys Leu Ile Val Val Glu
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 90
 95
- aac acc gcg gac acg cac aac gtg gtc gtg tgc acg ctg tgc tcg tgc 336
 Asn Thr Ala Asp Thr His Asn Val Val Cys Thr Leu Cys Ser Cys
- 40 tac ccg cgc atc ctg ctc ggc atc ccg ccc gag tgg tac aag tcg cgc 384

105

110

175

100

165

- Tyr Pro Arg Ile Leu Leu Gly Ile Pro Pro Glu Trp Tyr Lys Ser Arg 115 120 125
- 45 agc tac cgc agc cgc aca gtg cgc gag ccg cgc gcg gtg ctc gcc gaa 432
- Ser Tyr Arg Ser Arg Thr Val Arg Glu Pro Arg Ala Val Leu Ala Glu 130 135 140
- 50 ttc ggc acg acc atc ccg gag aac gtc gcg atc cga gtg cac gac agc 480
 - Phe Gly Thr Thr Ile Pro Glu Asn Val Ala Ile Arg Val His Asp Ser 145 150 155 160

170

act gcg gac atg cgc tac ctc gtg atg ccg atg cgg cct gcg ggc acc 528
Thr Ala Asp Met Arg Tyr Leu Val Met Pro Met Arg Pro Ala Gly Thr

42/75

gaa aat ttc acc gaa gag cag ctc gct gca ttg gtg acg cgc gac agc Glu Asn Phe Thr Glu Glu Gln Leu Ala Ala Leu Val Thr Arg Asp Ser ctg atc ggt gtt tcc tta gca acg ctt ccg tag Leu Ile Gly Val Ser Leu Ala Thr Leu Pro <210> <211> 202 <212> PRT <213> Unknown <220> Metagenome - alpha unit nitrile hydratase - M73dC9 <223> <400> Met Ser Ser Lys Pro Thr Glu Asp Leu Gly Thr Tyr Gln Pro Leu Thr Tyr Tyr Gln Met Met Glu Val Ser Leu Arg Glu Leu Leu Val Glu Lys Gly Val Ile Thr Glu Ala Glu Val Ala Arg Ala Met Gly Glu Ile Gly Ala Arg Ser Pro Glu Arg Gly Ala Lys Met Val Ala Arg Ala Trp Val Asp Pro Ala Tyr Lys Ala Arg Met Leu Ala Asp Gly Ser Lys Ala Ala Glu Glu Leu Gly Phe Glu Val Pro Gly Leu Lys Leu Ile Val Val Glu Asn Thr Ala Asp Thr His Asn Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Arg Ile Leu Leu Gly Ile Pro Pro Glu Trp Tyr Lys Ser Arg Ser Tyr Arg Ser Arg Thr Val Arg Glu Pro Arg Ala Val Leu Ala Glu Phe Gly Thr Thr Ile Pro Glu Asn Val Ala Ile Arg Val His Asp Ser

Thr Ala Asp Met Arg Tyr Leu Val Met Pro Met Arg Pro Ala Gly Thr 170 165 175

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gct gcc aac tgg caa ctt atc agt cgc cct tca tgg tca gct tgt aat

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Ala Ala Asn Trp Gln Leu Ile Ser Arg Pro Ser Trp Ser Ala Cys Asn 20 30 25

40 144

> Ile Leu Val Leu Met Ser Ala Thr His Pro Lys Lys Arg Ala Ala Asp 40 35

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45 192

Ile Gly Gly Asn Lys Ala Gly Ala Val Asp Thr Ala Asp His Gly Met 60 50 55

aag ttc tgg gag cgg cag gcc aac gcc ctg cgc acc gcg ctg cgg

50 240

Lys Phe Trp Glu Arg Gln Ala Asn Ala Leu Arg Thr Ala Leu Arg Arg 80 70 75 65

aat gga ctg atg agc gta gat gag ctg cgc cgc gca gcg gag gac ctg

55 288

Asn Gly Leu Met Ser Val Asp Glu Leu Arg Arg Ala Ala Glu Asp Leu 90 95 85

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1. 0	gcg 432	gcg	aag	atg	gcc	gag	gtg	cgg	aag	ccg	ctt	cga	tgt	gcc	gcg	caa
		Ala 130	Lys	Met	Ala	Glu	Val 135	Arg	Lys	Pro	Leu	Arg 140	Cys	Ala	Ala	Gln
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		Gly	Ile	Ala	Gly		Glu	Glu	Ser	Glu		Met	Asn	Pro	Ala	
20	145					150		<u>ـ</u> د ــد ـــ		.	155					160
	528		cag													
0.5	Gly	Lys	Gln	Asp	G1y 165	GIN	Arg	Leu	Pro	170	'I'nr	л Х т.	'I'nr	Ala	175	Pro
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	576 Gly	His	Arg	Phe 180	Asp	Val	Gly	Asp	Arg 185	Val	Val	Val	Lys	Arg 190	Ser	Asn
30	aaa	aaa	ggc		aaa	מממ	acc	aat		tac	atc	cac	aac	-	aca	aac
	624															
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	720 Tyr 225	Gly	Phe	Asp	Gly	Glu 230	Pro	Lys	Lys	Val	Leu 235	Tyr	Arg	Val	Arg	Phe 240
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	768 Arg	Gln	Lys	Glu		Trp	Pro	Ala	Tyr	Arg 250	Gly	Pro	Ala	His	Asp 255	Val
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	816		atg													
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Pro Pro Gly His Arg Arg Thr Pro His Tyr Ile Arg Gly Lys Thr Gly 205 195 200 5 Val Ile Glu Arg Ile Cys Gly Ala Phe Pro Asn Pro Glu Glu Leu Ala 220 210 215 Tyr Gly Phe Asp Gly Glu Pro Lys Lys Val Leu Tyr Arg Val Arg Phe 10 235 240 225 230 Arg Gln Lys Glu Val Trp Pro Ala Tyr Arg Gly Pro Ala His Asp Val 15 250 255 245 Ile Glu Met Glu Ile Phe Glu His Trp Leu Glu Pro Ala Gln Ser Gln 270 265 260 20 Lys Thr 25 <210> 63 <211> 627 <212> DNA <213> Unknown 30 <220> Metagenome - beta unit nitrile hydratase - M12K24 <223> <220> <221> 35 CDS <222> (1)..(627)<223> <400> 63 atg gac ggc atg cac gac ctg gga ggc agg cag ggc ttc gga ccg gtt 40 48 Met Asp Gly Met His Asp Leu Gly Gly Arg Gln Gly Phe Gly Pro Val 15 10 cgc tac acg atc gac gcg ccc gca ttc cat tcg ccg tgg gaa gtg cgc 45 96 Arg Tyr Thr Ile Asp Ala Pro Ala Phe His Ser Pro Trp Glu Val Arg 25 30 20 gcg aat tcg ctc tat gcg ttc gcg gtg cgc ctc ggc atc ttc aac atg 50 144 Ala Asn Ser Leu Tyr Ala Phe Ala Val Arg Leu Gly Ile Phe Asn Met 40 45 · 35

gac gaa tac cgc cat gcg atc gag cgg atg gag ccg cgc cat tac ctc

Asp Glu Tyr Arg His Ala Ile Glu Arg Met Glu Pro Arg His Tyr Leu

55

60

55

192

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	Thr 145	Gly	Val	Val	Val	Ser 150	Glu	Ser	Pro	Asp	Tyr 155	Pro	Phe	Pro	Asp	Ala 160
40	His	Ala	His	Ser	Val 165	Asp	Ala	Gln	Asp	Glu 170	Pro	Thr	Tyr	Asp	Val 175	Arg
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Arg Arg Glu Glu Asn Glu Pro Ala Phe His Glu Pro Trp Glu Gly Arg 20 25 30

gtt ttc gct ctg acc acg gcg gtc gag gcc tgg ggt cgg tgg acc ctc

144

Val Dho Ala Leu Thr Thr Ala Val Glu Ala Tro Gly Arg Tro Thr Leu

Val Phe Ala Leu Thr Thr Ala Val Glu Ala Trp Gly Arg Trp Thr Leu

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gat gct tcc cga cac cgg atc gag cgg atg aat gcg gcg gac tat ctg
192

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cgg gtg agc tat tac gag aag tgg ctc gag tcg ctt ctc gct ctc ctg 240

Arg Val Ser Tyr Tyr Glu Lys Trp Leu Glu Ser Leu Leu Ala Leu Leu 65 70 75 80

tcc gag acc gga atg gcg agt ccg gcg gag ata cgg agt ggg gag cgt 288

35 Ser Glu Thr Gly Met Ala Ser Pro Ala Glu Ile Arg Ser Gly Glu Arg 85 90 95

40 Ala Asp Gly Thr Pro Lys Ala Thr Pro Pro Leu Pro Ala Asp His Val 100 105 110

acg gcg att ctc gcc agc ggg ttt ccc gcg agc cgg gag gcg gga gct 384

Thr Ala Ile Leu Ala Ser Gly Phe Pro Ala Ser Arg Glu Ala Gly Ala 115 120 125

gcg cct cgc ttc cga gtg agc gag cgg gtg cgc acc cgg aac atc aac 432

50 Ala Pro Arg Phe Arg Val Ser Glu Arg Val Arg Thr Arg Asn Ile Asn 130 135 140

ccg acg act cac acg cgc ctt ccg cga tac gcc cgg cgg aag ctc ggg 480

Pro Thr Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Arg Lys Leu Gly 145 150 155 160

acg atc gag cgc gac cac gga gtg ttc gtc ttc ccg gat acg aac gcg 528

Thr Ile Glu Arg Asp His Gly Val Phe Val Phe Pro Asp Thr Asn Ala cac gct ctc ggg gag aaa ccg cag cac gtc tat tcg gtt cgt ttc gag His Ala Leu Gly Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Glu gcg cgt gag ctc tgg ggc gag act gcc agg cca gag gat tcc gtc tac Ala Arg Glu Leu Trp Gly Glu Thr Ala Arg Pro Glu Asp Ser Val Tyr atc gat ctt tgg gac gag tac ctt gaa ccc gtg tag Ile Asp Leu Trp Asp Glu Tyr Leu Glu Pro Val <210> <211> 219 <212> PRT <213> Unknown <220> Metagenome - beta unit nitrile hydratase - M29M24 <223> <400> 66 Met Asn Gly Val His Asp Met Gly Gly Met His Gly Met Gly Ala Ile Arg Arg Glu Glu Asn Glu Pro Ala Phe His Glu Pro Trp Glu Gly Arg Val Phe Ala Leu Thr Thr Ala Val Glu Ala Trp Gly Arg Trp Thr Leu Asp Ala Ser Arg His Arg Ile Glu Arg Met Asn Ala Ala Asp Tyr Leu Arg Val Ser Tyr Tyr Glu Lys Trp Leu Glu Ser Leu Leu Ala Leu Leu Ser Glu Thr Gly Met Ala Ser Pro Ala Glu Ile Arg Ser Gly Glu Arg Ala Asp Gly Thr Pro Lys Ala Thr Pro Pro Leu Pro Ala Asp His Val Thr Ala Ile Leu Ala Ser Gly Phe Pro Ala Ser Arg Glu Ala Gly Ala

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35404550	<220 <223 <222 <223 <400 at8 Met 1 gtc yal cgg 144)> i)> i)> i !> i 3> i acc Thr gag Glu	Tetago CDS (1) Taat Asn CCC	genom tcg Ser gag Glu 20	ctg Leu 5 ccg Pro	cac His aac Asn	gac Asp gag Glu	atg Met ccg Pro	ggc Gly ccg Pro 25	ggc Gly 10 ttt Phe	atg Met cac His	cac His cag Gln	ggc Gly cgc Arg	ttt Phe tgg Trp 30	Gly 15 gag Glu tgg	Arg ggc Gly acc
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- Thr Val Glu Ala Val Arg Gly Val His Val Phe Pro Asp Thr Ala Ala 45 165 170 175
- Leu Gly Ala Gly Asp Asp Pro Gln Trp Leu Tyr Ala Val Val Phe Pro 180 185 190
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Ala Arg Phe Ala Val Gly Glu Arg Val Arg Thr Arg Asn Ile His Pro

135

130

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Asp Leu Arg Pro Gln Pro Gln Pro Arg Phe Ala Val Gly Asp Arg Val 115 120 125 5 Val Val Arg Asp Ile His Pro Ala Gly His Thr Arg Val Pro Arg Tyr 130 135 140 Val Arg Gly Lys Arg Gly Thr Val Val His Val Ala Pro Lys Phe Ser 10 145 150 155 160 Phe Pro Asp Thr Ala Ala His Gly Leu Thr His Arg Ser Glu His Thr 165 170 175 15 Tyr His Val Glu Phe Val Ala Ser Asp Leu Trp Ala Asp Val Ala Gly 180 185 190 20 Ser Asn Glu Ser Val Leu Val Asp Leu Trp Asp Gly Tyr Leu Glu Gly 195 200 205 25 Ala <210> 75 30 <211> 651 <212> DNA <213> Unknown <220> 35 <223> Metagenome - beta unit nitrile hydratase - M25A18 <220> <221> CDS (1)..(651)<222> 40 <223> <400> 75 atg cgc ggc acg cac gat ctc ggc gga ttg ccc gcc ggc ccg gtg gac 48 45 Met Arg Gly Thr His Asp Leu Gly Gly Leu Pro Ala Gly Pro Val Asp 15 10 acc gct ccc cac gaa ccg acc ttc tgg gaa aag cag gtg gac gcg atc 96 50 Thr Ala Pro His Glu Pro Thr Phe Trp Glu Lys Gln Val Asp Ala Ile 20 25 30 cac ggc ctg ctc ggc gat tcc aag cgc cgc atc acg ctg cgc gac gag 144 55 His Gly Leu Leu Gly Asp Ser Lys Arg Arg Ile Thr Leu Arg Asp Glu 40 45 35 aac cgc ctc tat atc gaa tcg ctc ggc gac gac gtc tac aac acg ctc 192

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		130					135					140				
	_	acc	cat	acg	cgc	ctg	ccc	cgt	tac	gcg	cgc	ggc	aaa	ttc	ggc	gtt
5	480 Val 145	Thr	His	Thr	Arg	Leu 150	Pro	Arg	Tyr	Ala	Arg 155	Gly	Lys	Phe	Gly	Val 160
	atc 528	gaa	cgt	gac	cac	ggt	gtt	tac	agg	ttc	gac	gat	tcc	ttt	gcc	acg
10		Glu	Arg	Asp	His 165	Gly	Val	Tyr	Arg	Phe 170	Asp	Asp	Ser	Phe	Ala 175	Thr
	tcc 576	ggc	gac	gag	aag	ccc	cag	cac	gtt	tat	tct	gtg	cgc	ttc	gcg	gcg
15	Ser	Gly	Asp	Glu 180	Lys	Pro	Gln	His	Val 185	Tyr	Ser	Val	Arg	Phe 190	Ala	Ala
	cgc 624	gaa	cta	tgg	ggc	gaa	gcc	gcg	ccg	ccg	cga	gat	gct	gtc	tat	atc
20	Arg	Glu	Leu 195	Trp	Gly	Glu	Ala	Ala 200	Pro	Pro	Arg	Asp	Ala 205	Val	Tyr	Ile
	gaa 657	atc	tgg	gat	gac	aac	ctt	gag	cca	gcg	tga					
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Lys Gly Ala Ala Lys Ser Thr Pro Ala Ile Thr Ala Ala Thr Ala Gln Ala Tyr Met Phe Ala Leu Lys Ser Thr Arg Arg Asp Val Pro Val Thr Ala Arg Phe Gln Val Gly Gln Arg Val Arg Ala Arg Asn Ile Asn Pro Val Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Phe Gly Val Ile Glu Arg Asp His Gly Val Tyr Arg Phe Asp Asp Ser Phe Ala Thr Ser Gly Asp Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Ala Ala Arg Glu Leu Trp Gly Glu Ala Ala Pro Pro Arg Asp Ala Val Tyr Ile Glu Ile Trp Asp Asp Asn Leu Glu Pro Ala <210> 79 <211> 696 <212> DNA <213> Unknown <220> <223> Metagenome - beta unit nitrile hydratase - M3aG10 <220> <221> CDS <222> (1)..(696)<223> <400> 79 atg gat cca acg agg cgt agt ttc ctg gcg tct acc gtt gcc ctg acc Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr ggc ggc gca gct atc ccc gat ctg gct cat gcg gca gac cac gac cac Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His

cag cat caa gat ttg ccg tcc gat ctg gcg ctg cgg gtg aag tcg ctc Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu gaa tcg ctg ctt gtc gag aag ggg ctg gtg gag cga gca gcg ctc gac Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp gcg ctg gtg gac acc tac gag cac aaa gtc ggg ccg cga aac gga gcg Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala cgc gtt gtc gcg cgg gcc tgg gtt gac ccg gac tac aag caa cgg tta Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu ttc gcg aac ggt acc gcc gca gtc gcg gag ttc ggc tac tcc ggc tcg Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser cag ggc gct gac atc cgg gtc gtc gaa aac acg gcc act gta cat aac Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn ctc gtc gtg tgc acg ctg tgc tct tgt tat ccc tgg ccg gtg ctg ggc Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly ttg ccg ccg gtc tgg tac aag tcc gcg ccc tat cgg tct cgc gtg gtg Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val atc gat ccg cga ggt gtg ctg cgc gag ttc ggc gtg gtg ctg ccg gac Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp cat atc gaa gtg cgt gtc tat gac agc acg gcg gag caa cgc tat cta His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu gtg ctg ccg gag cgg ccg gcc gga acc gaa aac ctg aca gaa gaa gcg Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala ctg gcg ctg ctg gtg acg cgc gac gcg atg att ggc gtg gcc aag gtc Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val

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Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp

His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu 185 190 180 5 Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala 195 200 205 10 Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val 210 215 220 15 Ala Pro Pro Gly Gly Arg Gly 230 225 <210> 81 20 <211> 327 <212> DNA <213> Unknown <220> 25 <223> Metagenome - p12K unit <220> <221> CDS (1)..(327)<222> 30 <223> <400> 81 atg aaa gat agc ccg gtc ttt cgc gag ccg tgg gaa gcg cag gcg ttt 35 Met Lys Asp Ser Pro Val Phe Arg Glu Pro Trp Glu Ala Gln Ala Phe 15 10 gcg ttg gcg atc tcg ttg caa gac cgt ggc gtg ttc acg cga gac gaa 96 Ala Leu Ala Ile Ser Leu Gln Asp Arg Gly Val Phe Thr Arg Asp Glu 40 30 25 20 tgg gcg gcg gca ctc ggc gat gaa atc aag aag gcg caa gct gcc ggc 144 Trp Ala Ala Leu Gly Asp Glu Ile Lys Lys Ala Gln Ala Ala Gly 45 40 45 35 gat ccc gat acg ggc gag act tat tac cat cat tgg atg gca gcg ctc 192 Asp Pro Asp Thr Gly Glu Thr Tyr Tyr His His Trp Met Ala Ala Leu 50 50 55 60 gaa cgg ctg att gca gcc aag ggt gtt gcc gat acg cag acg ctc gcg 240 Glu Arg Leu Ile Ala Ala Lys Gly Val Ala Asp Thr Gln Thr Leu Ala 55 80 75 65 70 cgc aca cgc gac gcc tgg cag' cac gcc tgt gcg cga acg ccg cat ggc 288

Arg Thr Arg Asp Ala Trp Gln His Ala Cys Ala Arg Thr Pro His Gly 85 90 95

gcg cca atc gag cta aga ccg gac gac ttc agg aat tga 5 327

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Trp Ala Ala Leu Gly Asp Glu Ile Lys Lys Ala Gln Ala Ala Gly 35 40 45

30

Asp Pro Asp Thr Gly Glu Thr Tyr Tyr His His Trp Met Ala Ala Leu 50 60

35
Glu Arg Leu Ile Ala Ala Lys Gly Val Ala Asp Thr Gln Thr Leu Ala
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- 5
 Asp Ala Arg Gly Glu His Thr Ser Tyr Tyr Glu Arg Phe Leu Ala Ala
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 75
 80
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- Asp Leu Pro Gln Leu Pro Ser Asp Thr Asp Gly Pro Val Phe Ala Glu 20 25 30
 - cct tgg gaa gcg gaa gcg ttt gcg ctt gcc gta agt ctt tca gag caa
- Pro Trp Glu Ala Glu Ala Phe Ala Leu Ala Val Ser Leu Ser Glu Gln 45 45
 - gga cat ttc acg tgg aag gaa tgg gca gca acg ctc gcc gat gaa ctg 192
- Gly His Phe Thr Trp Lys Glu Trp Ala Ala Thr Leu Ala Asp Glu Leu 50 55 60
 - gag ggc gcc gcc aat cgc ggc gag ccg gat gac ggt acg cat tat tat 240
- Glu Gly Ala Ala Asn Arg Gly Glu Pro Asp Asp Gly Thr His Tyr Tyr 55 65 70 75 80
 - gag tac tgg ctg acg gcc ctg gaa agg ctg gtt acg atc aag ggc ctg 288
 - Glu Tyr Trp Leu Thr Ala Leu Glu Arg Leu Val Thr Ile Lys Gly Leu

aca gat cag caa gcg atg cgc gag cgc aaa gag gcg tgg gaa gaa gcc Thr Asp Gln Gln Ala Met Arg Glu Arg Lys Glu Ala Trp Glu Glu Ala tat cgc cat acc ccg cat ggc gcg cca gtt gaa ctt atg tct ccg ctc Tyr Arg His Thr Pro His Gly Ala Pro Val Glu Leu Met Ser Pro Leu gat caa agc cgg ata gcc gaa gag gac agc gaa tcc tca tag Asp Gln Ser Arg Ile Ala Glu Glu Asp Ser Glu Ser Ser <210> 86 <211> <212> PRT Unknown <213> <220> <223> Metagenome - p12K unit <400> Met Thr Thr Leu Ser Gln Arg Glu Ala Ala Pro Ser Ala Glu Leu Leu Asp Leu Pro Gln Leu Pro Ser Asp Thr Asp Gly Pro Val Phe Ala Glu Pro Trp Glu Ala Glu Ala Phe Ala Leu Ala Val Ser Leu Ser Glu Gln Gly His Phe Thr Trp Lys Glu Trp Ala Ala Thr Leu Ala Asp Glu Leu Glu Gly Ala Ala Asn Arg Gly Glu Pro Asp Asp Gly Thr His Tyr Tyr Glu Tyr Trp Leu Thr Ala Leu Glu Arg Leu Val Thr Ile Lys Gly Leu Thr Asp Gln Gln Ala Met Arg Glu Arg Lys Glu Ala Trp Glu Glu Ala Tyr Arg His Thr Pro His Gly Ala Pro Val Glu Leu Met Ser Pro Leu

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Asp Gln Ser Arg Ile Ala Glu Glu Asp Ser Glu Ser Ser 130 135 140

130 135 140